

## Claims

1. A constraint-based method for identifying a genomic target of interest from gene expression profiles, comprising:  
obtaining tissue sample expression data sets;  
selecting a working gene-expression set, said gene-expression set having a plurality of members;  
defining subgroups of said tissue samples of said expression data sets, wherein said subgroup definition is a constrained definition; and  
analyzing co-expression of said members of said working gene set across said subgroups and identifying potential gene targets.

2 The method of claim 1, wherein said tissue sample expression data sets are comprised of expression data sets from tumor samples.

3 The method of claim 1, wherein said tissue sample expression data sets are comprised of expression data sets from tissue from a mammal.

4 The method of claim 3, wherein said tissue sample expression data sets are comprised of expression data sets attained tissue from at least one of a human, mouse, primate, canine, pig, rat, and feline.

5 The method of claim 1, wherein said tissue sample expression data sets are comprised of expression data sets based upon tissue from an embryo.

6 The method of claim 2, wherein said tumor are breast cancer tumors.

7 The method of claim 2 wherein said tumors are cancer tumors of the digestive tract.

8 The method of claim 1, wherein said working gene expression set comprises at least one receptor tyrosine kinase.

9 The method of claim 1, wherein said working gene expression set comprises a receptor and a ligand.

10 The method of claim 1, further comprising a step of selecting known prognostic markers that are correlative with prognostic outcomes.

11. The method of claim 1, further comprising a step of binning said working gene-expression set.

12. A constraint-based method for analysis of gene expression profiles, comprising:

- selecting a working gene set;
- investigating expression patterns of said working gene set in a set of tissue samples;
- defining cutting values to define categories of gene expression levels;
- selecting constraints in order to bin said tissue samples into groups according to gene expression;
- investigating the frequency of up-regulated and down-regulated genes across individual members and groups; and
- forming at least one matrix which provides a basis for investigation of expression of members of said working gene set across said set of tissue samples, thereby providing at least one potential gene target.

13. The method of claim 12, wherein said investigation includes calculating an intensity ratio of a particular gene of said working gene set, said intensity ratio calculated by comparison of a particular gene expression intensity to a calculated average intensity.

14. The method of claim 13, wherein said intensity ratio is utilized to provide information utilized to construct at least a part of at least one matrix, said matrix being comprised of a plurality of calculated ratios.